REMARKS

Status of the Claims

Claims 8-11, 13-17, and 19-49 have been canceled, and claims 1 and 12 have been amended. Accordingly, claims 1-7, 12, and 18 will be pending upon entry of the instant amendment. Support for these amendments can be found throughout the specification and claims as originally filed. Specifically, support may be found, for example, at page 17, paragraph [0061]; at page 20, paragraph [0075]; and at page 22, paragraph [0086].

No new matter has been added by way of amendment, and Applicants submit that in view of the following remarks, the application is now in condition for allowance.

The Examiner's comments in the Office Action are addressed below in the order set forth therein.

The Rejection of Claims 1, 3-7, 12, and 18 Under 35 USC §112, Second Paragraph Should Be Withdrawn

Claims 1, 3-7, 12, and 18 are rejected under 35 USC §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Examiner asserts that the terms "stringent conditions" and "naturally occurring allelic variant" are unclear.

This rejection is respectfully traversed. However, in an effort to expedite prosecution, Applicants have amended Claims 1 and 12 to remove reference to both "stringent conditions" and "allelic variants" by deleting the corresponding subparts, claim 1e and claim 12c. In light of these amendments, the rejection of claims 1, 3-7, 12, and 18 under 35 USC §112, second paragraph, is believed to be moot. Applicants respectfully request reconsideration and withdrawal of this rejection.

The Rejection of Claims 1, 3-7, 12, and 18 Under 35 USC §112, First Paragraph (Enablement) Should Be Withdrawn

Claims 1, 3-7, 12, and 18 are rejected under 35 USC §112, first paragraph, because the specification, while being enabling for isolated nucleic acid molecules encoding ATM related kinase of SEQ ID NO:2, does not enable to one of skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claims. The Examiner asserts that the application does not provide enablement for the following:

> "(a) isolated nucleic acid molecules comprising a DNA sequence which is at least 60% identical to SEQ ID NO:1 and 3, with no function.
>
> (b) isolated nucleic acid molecules which comprise at least 300 nucleotides of SEQ ID NO:1 or 3, and isolated nucleic acid molecules encoding a fragment of SEQ ID NO:2, wherein said fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2 (wherein said DNA fragment must inherently comprise (15x3) 45 bases of said DNA sequences) with no function.

(c) isolated nucleic acid molecules encoding a 'naturally occurring allelic variants' of SEQ ID NO:2, wherein the molecule hybridizes with a DNA molecule comprising SEQ ID NO:1, 3, or complement thereof, under stringent conditions, with no function."

The Examiner asserts that the specification fails to provide sufficient guidance or provide examples which teach which residues in the molecule of the present application may be altered while still encoding products supported by the specification. This rejection is respectfully traversed.

The Examiner initially concedes that the specification is enabling for isolated nucleic acid molecules encoding the full-length kinase of SEQ ID NO:2, including SEQ ID NO:1 and 3. However, the Examiner cites *In re Wands* and concludes that the amount of experimentation required to determine the specific nucleotides which may be changed in SEQ ID NO:1 or 3 to still encode products that are within the scope of the present invention "(i.e. retain kinase activity)" is undue.

Currently amended claims 1 and 12 recite: 1) nucleic acid molecules at least 95% identical to SEQ ID NO:1 or 3, wherein the polypeptide encoded by the nucleic acid has kinase activity; 2) fragments comprising at least 1400 contiguous nucleotides of SEQ ID NO:1 or 3, wherein the recited fragments have kinase activity; 3) nucleic acid molecules encoding the polypeptide sequence of SEQ ID NO:2; and 4) fragments of SEQ ID NO:2 comprising at least 1000 contiguous amino acids, wherein the recited fragments have kinase activity. The limitations within these amended claims are fully enabled within the specification as Applicants have provided teachings for every necessary element for one of skill in the art to practice the claimed invention.

In contrast to the Examiner's assertions, guidance is provided as to which regions of the sequence of 13245 may be altered and still encode a polypeptide encompassed by the claims.

First, Applicants have provided the 13245 nucleotide sequences in SEQ ID NO:1 and 3. The claimed sequences of the invention vary from this sequence by structural parameters (*e.g.* percent sequence identity to SEQ ID NO:1). Guidance for determining percent sequence homology is provided in the specification on page 17, paragraph [0062] to page 19, paragraph [0066].

Moreover, the polypeptides encoded by the sequences of claims 1a, 1b, 1d, and 12b retain kinase activity and therefore encompass functional variants. Guidance regarding alterations that allow the sequence to retain kinase activity is also provided. See, for example, pages 16-17, paragraph [0059] and page 24, paragraph [0095] that provide guidance regarding conservative substitutions of amino acids in generating functional variants.

Further, the specification discloses conserved regions of the 13245 sequence of the present invention. For example, the specification at page 10, paragraphs [0038] and [0039]; and page 30, paragraph [114] teaches specific regions of the polypeptide sequence of 13245 critical for kinase activity, as well as how variants may differ from SEQ ID NO:2 and still retain kinase function.

Finally, methods for making variant sequences are routine in the art, as are those for assaying kinase activity. Accordingly, one of skill in the art would be able to generate sequences encompassed by the claims of this invention (*e.g.* 1) nucleic acid molecules at least 95% identical to SEQ ID NO:1 or 3, wherein the polypeptide encoded by the nucleic acid has kinase activity; 2) fragments comprising at least 1400 contiguous nucleotides of SEQ ID NO:1 or 3, wherein the recited fragments have kinase activity; 3) nucleic acid molecules encoding the polypeptide sequence of SEQ ID NO:2; and 4) fragments of SEQ ID NO:2 comprising at least 1000 contiguous amino acids, wherein the recited fragments have kinase activity), and determine if the variant sequences retain kinase activity.

Thus, a rational scheme for determining the regions of the recited 13245 kinase polypeptide encoded by the claimed sequences that would tolerate modification is provided. Based on the guidance regarding the conserved consensus sequences of the kinase polypeptide, and the methods for identifying additional residues critical for kinase function, the skilled artisan could choose among possible modifications to produce polypeptides encoded by nucleotides within the parameters set forth in the claims and test these modified variants to determine if they retain kinase activity.

Therefore, Applicants have provided all of the necessary information to enable one of skill in the art to 1) identify regions within the polynucleotide of the claimed invention which may be altered while maintaining activity; 2) generate fragments or variants; and 3) perform assays to determine whether or not the sequences generated do in fact have the desired kinase activity. Consequently, contrary to the Examiner's conclusions, the quantity of experimentation necessary is not undue, and the guidance presented in the specification is sufficient to enable the claimed polynucleotides, methods and kits as set forth in claims 1, 3-7, 12, and 18.

Applicants have provided sufficient guidance to enable one of skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the amended claims 1 and 12 and their dependent claims. Applicants respectfully request reconsideration and withdrawal of the rejection of claims 1, 3-7, 12, and 18 under 35 USC §112, first paragraph (enablement).

The Rejection of Claims 1, 3-7, 12, and 18 Under 35 USC §112, First Paragraph (Written Description) Should Be Withdrawn

Claims 1, 3-7, 12, and 18 are rejected under 35 USC §112, first paragraph, as failing to comply with the written description requirement. The Examiner asserts that claims 1 and 12 (and their dependent claims 3-7 and 18) are directed to the following genera of DNA sequences that have been inadequately described in the specification:

"(a) a genus of isolated nucleic acid molecules comprising a DNA sequence which is at least 60% identical to SEQ ID NO:1 and 3, with no function.

(b) a genus of isolated nucleic acid molecules which comprise at least 300 nucleotides of SEQ ID NO:1 and 3, and a genus of isolated nucleic acid molecules encoding a fragment of SEQ ID NO:2 wherein said fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2 (wherein said DNA fragment must inherently comprise (15x3) 45 bases of said DNA sequences) with no function.

(c) a genus of isolated nucleic acid molecules encoding a fragment of SEQ ID NO:2, wherein said fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, with no function.

(d) a genus of isolated nucleic acid molecules encoding naturally occurring allelic variants of SEQ ID NO:1 or 3, that hybridize to SEQ ID NO:1 or 3, under stringent conditions, comprising numerous embodiments with no function."

Applicants respectfully traverse this rejection, however in the interest of expediting prosecution, and in no way acquiescing to the Examiner's rejection, Applicants have amended claims 1 and 12.

As stated above, newly amended claims 1 and 12 recite: 1) nucleic acid molecules at least 95% identical to SEQ ID NO:1 or 3, wherein the polypeptide encoded by the nucleic acid has kinase activity; 2) fragments comprising at least 1400 contiguous nucleotides of SEQ ID NO:1 or 3, wherein the recited fragments have kinase activity; 3) nucleic acid molecules encoding the polypeptide sequence of SEQ ID NO:2; and 4) fragments of SEQ ID NO:2 comprising at least 1000 contiguous amino acids, wherein the recited fragments have kinase activity. In light of these currently amended claims, Applicants traverse the Examiner's rejection and argue that they were in possession of the claimed invention at the time of filing for the reasons discussed below.

Contrary to the Examiner's assertion, the specification not only provides the sequence of the claimed polynucleotide and polypeptide encoded therefrom but also provides a fragment that falls within the scope of the new claims, namely the kinase domain, as well as extensive teachings as discussed above, to obtain other functionally active fragments which fall within the scope of the new claims. Therefore, by having provided the full length sequence of the claimed polynucleotide and polypeptide encoded therefrom, a functional fragment of the polypeptide of the claimed invention having the desired activity and an enabling disclosure for obtaining other such functional sequences, Applicants have provided the necessary teachings to demonstrate that they were in possession of the claimed invention at the time of filing. Applicants therefore respectfully request reconsideration and withdrawal of the foregoing 35 U.S.C. § 112, first paragraph rejection over claims 1, 3-7, 12 and 18.

The Rejection of Claims 1, 3-7, 12, and 18 Under 35 USC §102(b), Should Be Withdrawn

Claims 1, 3-7, 12, and 18 are rejected under 35 USC §102(b) as being anticipated by Di Cunto et al. (JBC 273(45), 29706-29711, 1998, cited in the IDS; GenBank accession 086824). The Examiner asserts that Di Cunto teaches a DNA sequence that can hybridize to SEQ ID NO:1 or 3 of this invention

under stringent conditions. The Examiner also asserts that Di Cunto teaches about recombinant plasmids and both COS cells and mouse keratinocytes comprising its DNA sequence, as well as a kit that comprises a cDNA that can hybridize to a fragment of SEQ ID NO:1 or 3 capable of encoding 15 contiguous amino acids of SEQ ID NO:2 or a fragment of SEQ ID NO:1 or 3, of 300 bases in length, under "stringent hybridization conditions", anticipating claim 18. This rejection is respectfully traversed.

The currently amended claims recite: 1) nucleic acid molecules at least 95% identical to SEQ ID NO:1 or 3, wherein the polypeptide encoded by the nucleic acid has kinase activity; 2) fragments comprising at least 1400 contiguous nucleotides of SEQ ID NO:1 or 3, wherein the recited fragments have kinase activity; 3) nucleic acid molecules encoding the polypeptide sequence of SEQ ID NO:2; and 4) fragments of SEQ ID NO:2 comprising at least 1000 contiguous amino acids, wherein the recited fragments have kinase activity.

Applicants have performed sequence alignments of the Di Cunto sequence with the sequences of SEQ ID NO:1 and 3, attached as Exhibit A, showing that the relative identity of the cited sequence is 71.3% identity to the entire length of SEQ ID NO:1 and 75.0% identity to the entire length of SEQ ID NO:3. The limitations within the currently amended claims (*e.g.* 95% identity) do not encompass the sequence of the Di Cunto reference. Therefore, the rejection of claims under 35 USC §102(b) is considered to be moot. Applicants respectfully request reconsideration and withdrawal of the rejection of claims 1, 3-7, 12, and 18 under 35 USC §102.

CONCLUSION

In view of the aforementioned amendments and remarks, Applicants respectfully submit that the rejections of the claims under 35 USC § 112 second paragraph, §112 first paragraph, and §102 are overcome. The Examiner is respectfully requested to withdraw the rejections and allow claims 1, 3-7, 12, and 18. In any event, entry of the above amendments for purposes of further prosecution is respectfully requested.

Accordingly, it is submitted that this application is now in condition for allowance. If, in the opinion of the Examiner, a telephone conference would expedite the prosecution of the subject application, the Examiner is invited to call the undersigned.

This paper is being filed timely as a request for a two month extension of time is filed concurrently herewith. No additional extensions of time are required. In the event any additional extensions of time are necessary, the undersigned hereby authorizes the requisite fees to be charged to Deposit Account No. 501668.

Entry of the remarks made herein is respectfully requested.

Respectfully submitted,

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